## COPCT Rec'd 13 NOV 200

PATENTS

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of

Anthony Keith CAMPBELL

Serial No. 09/831,142 (PCT/GB99/03654)

Box PCT

Attention: DO/EO

Filed May 7,2001

PROTEIN AND DNA CODING THEREFOR

### REQUEST FOR PERMISSION TO MAKE DRAWING CORRECTIONS

Commissioner for Patents

Washington, D.C. 20231

Sir:

Permission is respectfully requested to amend Figures 1, 2, 3, 4A and 4B, 5A and 5B, 6, 7A, 7B, 7C, and 9 as indicated in red on the accompanying prints.

Respectfully submitted,

& THOMPSON

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November 13, 2001

clone 40: (SEQ ID NO: 1)

GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT GGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA GATCGGGCTTTGGGGCTGTCGGATTGAACGGGCCCGGCCCAGGTACCAC AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA **AAAAAAAAAAAAACTCGAG** 

Clone 3: (FEQ ID NO:2)

GAATTCGGCACGAGGGAAAAGAACAAAATGGCTTGTATCGTTTCGTT GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA GACACAGTAGACGAGGCTGAAGACACCCGTCAGAAACTGGAGAATTCTT CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG ATAGAATATTGAAAATAA

Clone 5: (EQ 1) NO:3)

# Fig. 1

clone 40 clone 3 clone 5	GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT GAATTCGGCACGAGGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTTGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT
clone 40 clone 3 clone 5	GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 40	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 3	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 5	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 40	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
clone 3	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
clone 5	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAG
clone 40 clone 3 clone 5	GATCGGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCC
clone 40	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 3	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 5	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 40	GAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 3	GAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 5	GAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 40 clone 3 clone 5	TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
clone 40	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 3	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 5	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 40	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 3	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 5	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 40	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
clone 3	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT
clone 5	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTTAT
clone 40	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 3	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 5	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC

# Fig. 2 (Part 1 of 2)

clone 40	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 3	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 5	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 40	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 3	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 5	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 40	CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 3	CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 5	CTGGTAGATCTATCAGACCACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 40	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 3	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 5	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG
clone 40 clone 3 clone 5	ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA ATAGAATATTGAAAATAA——————————
clone 40 clone 3 clone 5	AAAAAAAAAAAAAACTCGAG (SEQ ID NO: 1) AAAAAAAAAAAAAAACTCGAG (SEQ ID NO: 2)

Fig. 2 (Part 2 of 2)

GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTTGCTCTTG TCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACAATGCGCGATGAATT GGACACAAGCTAATGAATATGTGTTCAACGTGGACTGGATGACCATTTTCATCTACG ACTATGGCGCTCAAGAGCAACTGTACGAAGATCGGGCTTTGGGGCTGTCGGATTG AACGGGCCGGCCCAGGTACCACAAAAGCCGTCTGGATTAACTGGAGTAACGACACGC AGTCATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGC TAGTTGACTACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCT CTAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGGACGCTG ATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTGTCCCTATATGACG AAGATAACAATGGTGTAATGGATGAAGGTAAGGTGTTCCATCTGAGACAATCGAGGA TGATATCAAGGACTGTGGGCTCTTAGACCAAGATGTTGAACTCGATTATACGTGGAC TCAAAACGAGTGTGATCTACCAGACACAGTAGACGAGGCTGAAGACACACCGTCAGA **AACTGGAGAATTCTTCTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGG** TCGTTACCAGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATC **AAAAAAAACTCGAG** 

Fig. 3 (50 0 10 No. 1)

GAA:	rrcgo				\AAG#	VYCY	A.A.									
		_		GTT V	TTC F	GTT V	GCT A	CTT L	GTC V	GCT A	CTA L	TGC C	TTA L	atg M		45
CAA Q	CCG P	GGT G	TCC S	GGT G	GAG E	gaa E	GTA V	CAA Q	TGC C	GCG A	atg M	AAT N	TGG W	ACA T		90
CAA Q	GCT A	aat N	gaa E	TAT Y	GTG V	TTC F	aac N		GAC D	TGG W	ATG M	ACC T	att I	TTC F		135
atc I	TAC Y	GAC D	TAT Y	GGC G	GCT A	CAA Q	gag E	CAA Q	CTG L	TAC Y	GAA E	GAT D	CGG R	GCT A		180
TTG L	GGG G	CTG L	TGT C	CGG R	ATT I	GAA E	CGG R	GCC A	GGC G	CCA P	GGT G	ACC T	ACA T	aaa K		225
GCC A	GTC V	TGG W	att I	aac n	TGG W	agt s	AAC N	GAC D	ACG T	CAG Q	TCA S	TGT C	GTA V	ACA T	1	270
aga R	aaa K	ACA T	ATC I	TTC F	TTC F	GAG E	GTT V	GGT G	GGA G	gaa E	TTA I	GCC A ·	CGG R	CTA L		315
GTT V	GAC D	TAC Y	aga R	CCA P	CAG Q	gaa E	GAC D	GGA G	ACT T	gag E	AAA K	ACT T	TTT F	ACA T	;	360
AGA R	AAA K	TTC F	TCT ·	AGC S	AAA K	atg M	CCA P	GGC G	ACT T	TAC Y	atg M	CTT L	atg M	GAC D		405
gtg V	TGC C	gct A	ACA T	AGG R	GAC D	GCT A	GAT D	GAT D	AAA K	TGC C	ATC I	GAA E	GGC G	ACA T		450
att I	gtg V	GTG V	ACA T	GTC V	AGG R	GTG V	TCC S	CTA L	TAT Y	GAC D	GAA E	GAT D	aac n	AAT N		495
ggt G	gta V	atg M	gat D	gaa E	ggt g	aag K	gtg V	ATT I	CCA P	TCT S	gag e	aca T	ATC I	gag E		540
GAT D	GAT D	ATC I	aag K	GAC D	TGT C	GGG G	CTC L	TTA L	GAC D	CAA Q	GAT D	GTT V	gaa e	CTC		585
GAT D	TAT Y	ACG T	TGG W	ACT T	CAA Q	aac n	gag E	TGT C	GAT D	CTA L	CCA P	GAC D	aca T	GTA V		630
GAC D	GAG E	GCT A	GAA E	GAC D	ACA T	CCG P	TCA S	GAA E	ACT T	GGA G	GAA E	TTC F	TTC F	TGG W		675
TAG •	ATC	TAT	CAG	ACT	ACT	TTT	ATC	AGC	AGG	ACA	ACT	GG T	CGT	TAC		720
CAG	ACA	сст	ATA	ACG	TGT	CCT	CAT	CAA	TAA							750

Fig. 4A (SEQ ID NOS I and 4)

\* = stop for translation

EcoR I

#### GAATTCGGCACGAGTCGGAAAAGAACAAA

ATG GCT TGT ATC GTT TTC GTT GCT CTT GTC GCT CTA TGC TTA ATG CAA CCG GGT TCC GGT GAG GAA GTA CAA TGC GCG ATG AAT TGG ACA CAA GCT AAT GAA TAT GTG TTC AAC GTG GAC TGG ATG ACC ATT TTC ATC TAC GAC TAT GGC GCT CAA GAG CAA CTG TAC GAA GAT CGG GCT TTG GGG CTG TGT CGG ATT GAA CGG GCC GGC CCA GGT ACC ACA AAA GCC GTC TGG ATT AAC TGG AGT AAC GAC ACG CAG TCA TGT GTA ACA AGA AAA ACA ATC TTC TTC GAG GTT GGT GGA GAA ATT GCC CGG CTA GTT GAC TAC AGA CCA CAG GAA GAC GGA ACT GAG AAA ACT TTT ACA AGA AAA TTC TCT AGC AAA ATG CCA GGC ACT TAC ATG CTT ATG GAC GTG TGC GCT ACA AGG GAC GCT GAT GAT AAA TGC ATC GAA GGC ACA ATT GTG GTG ACA GTC AGG GTG TCC CTA TAT GAC GAA GAT AAC AAT GGT GTA ATG GAT GAA GGT AAG GTG ATT CCA TCT GAG ACA ATC GAG GAT GAT ATC AAG GAC TGT GGG CTC TTA GAC CAA GAT GTT GAA CTC GAT TAT ACG TGG ACT CAA AAC GAG TGT GAT CTA CCA GAC ACA GTA GAC GAG GCT GAA GAC ACA CCG TCA GAA ACT GGA GAA TTC TTC TGG TAG ATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACCAGAC ACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCGA TAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAA **AAAAAAAAAAAAAACTCGAG** 

Xho I

Fig. 4B (SEQ ID NO: 1)

EEVQCAMNWTQANEYVFNVDWMTIFIYDYGAQEQLYEDRALGLCRIERAGPGTTKAV WINWSNDTQSCVTRKTIFFEVGGEIARLVDYRPQEDGTEKTFTRKFSSKMPGTYMLM DVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEGKVIPSETIEDDIKDCGLLDQ DVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5A (SEQ ID NO:5)

MACIVFVALVALCLMQPGSGEEVQCAMNWTQANEYVFNVDWMTIFIYDYGAQEQLYE DRALGLCRIERAGPGTTKAVWINWSNDTQSCVTRKTIFFEVGGEIARLVDYRPQEDG TEKTFTRKFSSKMPGTYMLMDVCATRDADDKCIEGTIVVTVRVSLYDEDNNGVMDEG KVIPSETIEDDIKDCGLLDQDVELDYTWTQNECDLPDTVDEAEDTPSETGEFFW

Fig. 5B (5EQ 10 NO: 6)

clone 40 BioXAct rTth	GAATTCGGCACGAGTCGGAAAAGAACAAAATGGCTTGTATCGTTTTCGTT TGGCTTGTATCGTTTTCGTT
clone 40	GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
BioXAct	GCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
rTth	TATGCTTAATGCAACCGGGTTCCGGTGAGGAAGTACA
clone 40	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
BioXAct	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
rTth	ATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGACT
clone 40	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
BioXAct	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
rTth	GGATGACCATTTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAA
clone 40 BioXAct rTth	GATCGGCTTTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCAC GATCGGGCTTTGGGGCTGTGCGGATTGAACGGGCCGGCCCAGGTACCAC GATCGGGCTTTGGGGCTGTGCCGGATTGAACGGGCCGGCC
clone 40	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
BioXAct	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
rTth	AAAAGCCGTCTGGATTAACTGGAGTAACGACACGCAGTCATGTGTAACAA
clone 40	GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
BioXAct	GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
rTth	GAAAAACAATCTTCTTCGAGGTTGGTGGAGAAATTGCCCGGCTAGTTGAC
clone 40 BioXAct rTth	TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC TACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACAAGAAAATTCTC
clone 40	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
BioXAct	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
rTth	TAGCAAAATGCCAGGCACTTACATGCTTATGGACGTGTGCGCTACAAGGG
clone 40	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
BioXAct	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
rTth	ACGCTGATGATAAATGCATCGAAGGCACAATTGTGGTGACAGTCAGGGTG
clone 40	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
BioXAct	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
rTth	TCCCTATATGACGAAGATAACAATGGTGTAATGGATGAAGGTAAGGTGAT
clone 40	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
BioXAct	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC

# Fig. 6 (Part 1 of 2)

rTth	TCCATCTGAGACAATCGAGGATGATATCAAGGACTGTGGGCTCTTAGACC
clone 40 BioXAct rTth	AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA AAGATGTTGAACTCGATTATACGTGGACTCAAAACGAGTGTGATCTACCA
clone 40 BioXAct rTth	GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT GACACAGTAGACGAGGCTGAAGACACACCGTCAGAAACTGGAGAATTCTT
clone 40 BioXAct rTth	CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC CTGGTAGATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC CTGGTANATCTATCAGACTACTTTTATCAGCAGGACAACTGGTCGTTACC
clone 40 BioXAct rTth	AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAACAGAAATAATCG AGACACCTATAACGTGTCCTCATCAATAATGTGTAAAAC
clone 40 BioXAct rTth	ATAGAATATTGAAAATAAAATGTTAATAAACACTGGTTGAAATATGAAAA ATAGAATATTGAAAATAAAAT
clone 40 BioXAct rTth	AAAAAAAAAAAAAAAACTCGAG (SÉQID NO:1) (Quice of SEQID NO:1) (SEQID NO: 23)

Fig. 6 (Part 2 of 2)

Oligo 1

ACI ATH TTY TTY CAR GT

Oligo 2

CAR GAR GAR GGN ACI GA

Oligo 2A

TCI GTN CCY TCY TCY TG

Oligo N

TTY AAY GTI GAY TGG ATG

M=A/C

R=A/G K=G/T  $T \setminus A = W$ 

S=G/C

(=C/T

V=A/C/G H=A/C/T I=inosine

D=A/G/T B=C/G/T

=C/G/T N=A/C/G/T

Oligo 3A

ACA CAG CCC CAA AGC CCG AT

Oligo 4S

.TTG CCC GGC TAG TTG ACT AC

Oligo 5A

CAT ATT TCA ACC AGT GTT TAT TAA

Oligo 6A

CAA TTG TGC CTT CGA TGC A

Oligo 7S

GGA CTG TGG GCT CTT AG

Oligo 85

ATG GCT TGT ATC GTT TTC GT

Oligo T7

Oligo ExS

CCA CAC GGA TCC TGA GGA AGT ACA ATG

Oligo ExA

CCA CAC GGA TCC TTA TTG ATG AGG ACA

Oligo Bacl

CTT GTT TTT ATG GTC GTC TAC ATT TCT TAC ATC TAT GCG GAG GAA GTA CAA TG

Oligo C9 12

CCA CAC AGA TCT AGA ATG AAA TTC TTA GTC AAC GTT GCC CTT GTT TTT ATG GTC

## Oligo BV5

TTT ACT GTT TTC GTA ACA GTT TTG

### Oligo BV3

CAA CAA CGC ACA GAA TCT AG

Fig. 7C (SEQ ID NOS 17-22, respectively, in order of appearance)

```
NlaIV
                                                     MnlI
                                                   ScrFI
                                                   Ncil
                                                  BonI
                                                  Kpall Kpall
                                         MseI
                                                 ii ii i
   ATGGCTTGTATCGTTTCGTTGCTCTTGTCGCTCTATGCTTAATGCAACCGGGTTCCGGT
                  HhaI
            HphI BstUI
           RsaI HinPlI
                                   AluI
           11 11
                                   ł
GAGGAAGTACAATGCGCGATGAATTGGACACAAGCTAATGAATATGTGTTCAACGTGGAC
                                 HaeII
                                HhaI
                                                     DpnI
                 FokI
                              HinPlI
                                              RsaI SauJAI
                              1 11
                                              1 11
TGGATGACCATTTCATCTACGACTATGGCGCTCAAGAGCAACTGTACGAAGATCGGGCT 180
                              KaeIII
                             Sau96I
                             Cfr13I
                            NaeI
                                     RsaI
                                    NlaTV
                            HpaII
                           HaeIII BanI
                           Cfr10I ScrFI
                         Sau96I BstNI
                         Cfr13I EcoRII KpnI
    MboII
                         Asul Asul Asp718
                                                        MseI
                         1 111111 1 1 1 1
TTGGGGCTGTGTCGGATTGAACGGGCCGGCCCAGGTACCACAAAGGCCGTCTGGATTAAC 240
                         MaeIII
                                   MboII
   · MaeIII
                         NlaIII MboII MnlI TaqI
                         11
                                  1 1
                                          - 1
TGGAGTAACGACACGCAGTCATGTGTAACAAGAAAAACAATCTTCTTCGAGGTTGGTGGA 300
               MaeI
           ScrFI
           Ncil
           HpaII
                                              MboII
                    HincII
                                             DdeI
           1 1
                                             1 1
GAAATTGCCCGGCTAGTTGACTACAGACCACAGGAAGACGGAACTGAGAAAACTTTTACA
```

Fig. 9 (Part 1 of 2)